



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,337B

DATE: 08/11/2004

TIME: 16:45:31

Input Set : A:\71555107.app

Output Set: N:\CRF4\08112004\I674337B.raw

3 <110> APPLICANT: MORI, SATOSHI
 4 HIGUCHI, KYOKO
 5 SUZUKI, KAZUYA
 6 NISHIZAWA, NAOKO
 7 NAKANISHI, HIROMI
 9 <120> TITLE OF INVENTION: NICOTIANAMINE SYNTHASE AND GENE ENCODING THE SAME
 11 <130> FILE REFERENCE: 71526-55107
 13 <140> CURRENT APPLICATION NUMBER: 09/674,337B
 14 <141> CURRENT FILING DATE: 2001-07-26
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02305
 17 <151> PRIOR FILING DATE: 1999-04-30
 19 <150> PRIOR APPLICATION NUMBER: JP 10-137685
 20 <151> PRIOR FILING DATE: 1998-04-30
 22 <160> NUMBER OF SEQ ID NOS: 37
 24 <170> SOFTWARE: PatentIn Ver. 3.2
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 328
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Hordeum vulgare
 31 <400> SEQUENCE: 1
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 33 1 5 10 15
 35 Gly Ile Gln Ala Ala Ile Ala Glu Leu Pro Ser Leu Ser Pro Ser Pro
 36 20 25 30
 38 Glu Val Asp Arg Leu Phe Thr Asp Leu Val Thr Ala Cys Val Pro Pro
 39 35 40 45
 41 Ser Pro Val Asp Val Thr Lys Leu Ser Pro Glu His Gln Arg Met Arg
 42 50 55 60
 44 Glu Ala Leu Ile Arg Leu Cys Ser Ala Ala Glu Gly Lys Leu Glu Ala
 45 65 70 75 80
 47 His Tyr Ala Asp Leu Ala Thr Phe Asp Asn Pro Leu Asp His Leu
 48 85 90 95
 50 Gly Leu Phe Pro Tyr Tyr Ser Asn Tyr Val Asn Leu Ser Arg Leu Glu
 51 100 105 110
 53 Tyr Glu Leu Leu Ala Arg His Val Pro Gly Ile Ala Pro Ala Arg Val
 54 115 120 125
 56 Ala Phe Val Gly Ser Gly Pro Leu Pro Phe Ser Ser Leu Val Leu Ala
 57 130 135 140
 59 Ala His His Leu Pro Glu Thr Gln Phe Asp Asn Tyr Asp Leu Cys Gly
 60 145 150 155 160
 62 Ala Ala Asn Glu Arg Ala Arg Lys Leu Phe Gly Ala Thr Ala Asp Gly
 63 165 170 175
 65 Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr



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66	180	185	190														
68	Gln	Glu	Leu	Gly	Ala	Tyr	Asp	Val	Val	Phe	Leu	Ala	Ala	Leu	Val	Gly	
69																	
71	195		200													205	
72	Met	Ala	Ala	Glu	Glu	Lys	Ala	Lys	Val	Ile	Ala	His	Leu	Gly	Ala	His	
74	210															220	
75	225	Met	Val	Glu	Gly	Ala	Ser	Leu	Val	Val	Arg	Ser	Ala	Arg	Pro	Arg	Gly
77	230															235	
78	245	Phe	Leu	Tyr	Pro	Ile	Val	Asp	Pro	Glu	Asp	Ile	Arg	Arg	Gly	Phe	
80	260															250	
81	275	Glu	Val	Leu	Ala	Val	His	His	Pro	Glu	Gly	Gl	Val	Ile	Asn	Ser	Val
83	280															265	
84	290	Ile	Val	Ala	Arg	Lys	Ala	Val	Glu	Ala	Gln	Leu	Ser	Gly	Pro	Gln	Asn
86	295															285	
87	305	Gly	Asp	Ala	His	Ala	Arg	Gly	Ala	Val	Pro	Leu	Val	Ser	Pro	Pro	Cys
89	310															300	
90	315	Asn	Phe	Ser	Thr	Lys	Met	Glu	Ala	Ser	Ala	Leu	Glu	Lys	Ser	Glu	Glu
92	320																
93	325	Leu	Thr	Ala	Lys	Glu	Leu	Ala	Phe								
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98	<212>	TYPE:	DNA														
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101	<220>	FEATURE:															
102	<221>	NAME/KEY:	CDS														
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107																Met	
108																1	
110	gat	gcc	cag	aac	aag	gag	gtc	gct	ctg	atc	gag	aag	atc	gcc	ggt		
111	Asp	Ala	Gln	Asn	Lys	Glu	Val	Ala	Ala	Leu	Ile	Glu	Lys	Ile	Ala	Gly	
112																105	
114	5	10	15														
115	atc	cag	gcc	atc	gcc	gag	ctg	ccg	tcg	atc	gag	ccg	tcc	ccc	gag		
116	Ile	Gln	Ala	Ala	Ile	Ala	Glu	Leu	Pro	Ser	Leu	Ser	Pro	Ser	Pro	Glu	
118	20	25	30													153	
119	gtc	gac	agg	ctc	ttc	acc	gac	ctc	gtc	acg	gcc	tgc	gtc	ccg	ccg	agc	
120	Val	Asp	Arg	Leu	Phe	Thr	Asp	Leu	Val	Thr	Ala	Cys	Val	Pro	Pro	Ser	
122	35	40	45													201	
123	ccc	gtc	gac	gtg	acg	aag	ctc	agg	cac	cag	agg	atg	cg	gag		249	
124	Pro	Val	Asp	Val	Thr	Lys	Leu	Ser	Pro	Glu	His	Gln	Arg	Met	Arg	Glu	
126	50	55	60	65													
127	gct	ctc	atc	cgc	ttg	tgc	tcc	gcc	gag	ggg	aag	ctc	gag	g	cac		
128	Ala	Leu	Ile	Arg	Leu	Cys	Ser	Ala	Ala	Glu	Lys	Leu	Glu	Ala	His		
130	70	75	80														
131	tac	gcc	gac	ctg	ctc	gcc	acc	ttc	gac	aac	ccg	ctc	gac	ctc	ggc		
132	Tyr	Ala	Asp	Leu	Leu	Ala	Thr	Phe	Asp	Asn	Pro	Leu	Asp	His	Leu	Gly	
134	85	90	95													345	
135	ctc	ttc	ccg	tac	tac	agc	aac	tac	gtc	aac	ctc	agc	agg	ctg	gag	tac	393

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135 Leu Phe Pro Tyr Tyr Ser Asn Tyr Val Asn Leu Ser Arg Leu Glu Tyr
 136 100 105 110
 138 gag ctc ctg gcg cgc cac gtg ccg ggc atc gcg ccg gcg cgc gtc gcc 441
 139 Glu Leu Leu Ala Arg His Val Pro Gly Ile Ala Pro Ala Arg Val Ala
 140 115 120 125
 142 ttc gtc ggc tcc ggc ccg ctg ccg ttc agc tcg ctc gtc ctc gcc gcg 489
 143 Phe Val Gly Ser Gly Pro Leu Pro Phe Ser Ser Leu Val Leu Ala Ala
 144 130 135 140 145
 146 cac cac ctg ccc gag acc cag ttc gac aac tac gac ctg tgc ggc gcg 537
 147 His His Leu Pro Glu Thr Gln Phe Asp Asn Tyr Asp Leu Cys Gly Ala
 148 150 155 160
 150 gcc aac gag cgc gcc agg aag ctg ttc ggc gcg acg gcg gac ggc gtc 585
 151 Ala Asn Glu Arg Ala Arg Lys Leu Phe Gly Ala Thr Ala Asp Gly Val
 152 165 170 175
 154 ggc gcg cgt atg tcg ttc cac acg gcg gac gtc gcc gac ctc acc cag 633
 155 Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu Thr Gln
 156 180 185 190
 158 gag ctc ggc gcc tac gac gtg gtc ttc ctc gcc gcg ctc gtc ggc atg
 159 Glu Leu Gly Ala Tyr Asp Val Val Phe Leu Ala Ala Leu Val Gly Met
 160 195 200 205
 162 gca gcc gag gag aag gcc aag gtg att gcc cac ctg ggc gcg cac atg 729
 163 Ala Ala Glu Glu Lys Ala Lys Val Ile Ala His Leu Gly Ala His Met
 164 210 215 220 225
 166 gtg gag ggg gcg tcc ctg gtc gtg cgg agc gca cgg ccc cgc ggc ttt 777
 167 Val Glu Gly Ala Ser Leu Val Val Arg Ser Ala Arg Pro Arg Gly Phe
 168 230 235 240
 170 ctt tac ccc att gtc gac ccg gag gac atc agg cgg ggt ggg ttc gag 825
 171 Leu Tyr Pro Ile Val Asp Pro Glu Asp Ile Arg Arg Gly Gly Phe Glu
 172 245 250 255
 174 gtg ctg gcc gtg cac cac ccg gaa ggt gag gtg atc aac tct gtc atc 873
 175 Val Leu Ala Val His His Pro Glu Gly Glu Val Ile Asn Ser Val Ile
 176 260 265 270
 178 gtc gcc cgt aag gcc gtc gaa gcg cag ctc agt ggg ccg cag aac gga 921
 179 Val Ala Arg Lys Ala Val Glu Ala Gln Leu Ser Gly Pro Gln Asn Gly
 180 275 280 285
 182 gac gcg cac gca ccg ggc gcg gtg ccg ttg gtc agc ccg cca tgc aac 969
 183 Asp Ala His Ala Arg Gly Ala Val Pro Leu Val Ser Pro Pro Cys Asn
 184 290 295 300 305
 186 ttc tcc acc aag atg gag gcg agc gcg ctt gag aag agc gag gag ctg 1017
 187 Phe Ser Thr Lys Met Glu Ala Ser Ala Leu Glu Lys Ser Glu Glu Leu
 188 310 315 320
 190 acc gcc aaa gag ctg gcc ttt tga ttgaagagtgcgcgtggta ttctgtcgcc 1071
 191 Thr Ala Lys Glu Leu Ala Phe
 192 325
 194 tgcgatcggtg gtaactttcc tactcggtgt tggttgatg tttgtgcctg taagagttat 1131
 196 gcttccggcc ttgtgctgtt aatttacacg cgttacatgt agtacttgta ttatatacctg 1191
 198 gaataacggatgtgaaatattatgtggatttgaagtgtaatgcta aataataaga 1251
 200 aaacttggatc cagacattca aaaaaaaaaaaaaaaa aaaaaaaa 1295
 204 <210>. SEQ ID NO: 3

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205 <211> LENGTH: 335
 206 <212> TYPE: PRT
 207 <213> ORGANISM: Hordeum vulgare
 209 <400> SEQUENCE: 3

210 Met Ala Ala Gln Asn Asn Gln Glu Val Asp Ala Leu Val Glu Lys Ile
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 213 Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro Ser
 214 20 25 30
 216 Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr Ala Cys Val Pro
 217 35 40 45
 219 Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu Ala Gln Glu Met
 220 50 55 60
 222 Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu Gly Lys Leu Glu
 223 65 70 75 80
 225 Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp Lys Pro Leu Asp His
 226 85 90 95
 228 Leu Gly Met Phe Pro Tyr Tyr Asn Asn Tyr Ile Asn Leu Ser Lys Leu
 229 100 105 110
 231 Glu Tyr Glu Leu Leu Ala Arg Tyr Val Pro Gly Gly Tyr Arg Pro Ala
 232 115 120 125
 234 Arg Val Ala Phe Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Phe Val
 235 130 135 140
 237 Leu Ala Ala Arg His Leu Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu
 238 145 150 155 160
 240 Cys Gly Ala Ala Asn Asp Arg Ala Ser Lys Leu Phe Arg Ala Asp Arg
 241 165 170 175
 243 Asp Val Gly Ala Arg Met Ser Phe His Thr Ala Asp Val Ala Asp Leu
 244 180 185 190
 246 Ala Gly Glu Leu Ala Lys Tyr Asp Val Val Phe Leu Ala Ala Leu Val
 247 195 200 205
 249 Gly Met Ala Ala Glu Asp Lys Ala Lys Val Ile Ala His Leu Gly Ala
 250 210 215 220
 252 His Met Ala Asp Gly Ala Ala Leu Val Val Arg Ser Ala His Gly Ala
 253 225 230 235 240
 255 Arg Gly Phe Leu Tyr Pro Ile Val Asp Pro Gln Asp Ile Gly Arg Gly
 256 245 250 255
 258 Gly Phe Glu Val Leu Ala Val Cys His Pro Asp Asp Asp Val Val Asn
 259 260 265 270
 261 Ser Val Ile Ile Ala Gln Lys Ser Lys Asp Val His Ala Asp Gly Leu
 262 275 280 285
 264 Gly Ser Gly Arg Gly Ala Gly Gly Gln Tyr Ala Arg Gly Thr Val Pro
 265 290 295 300
 267 Val Val Ser Pro Pro Cys Arg Phe Gly Glu Met Val Ala Asp Val Thr
 268 305 310 315 320
 270 Gln Asn His Lys Arg Asp Glu Phe Ala Asn Ala Glu Val Ala Phe
 271 325 330 335
 274 <210> SEQ ID NO: 4
 275 <211> LENGTH: 1342
 276 <212> TYPE: DNA

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Input Set : A:\71555107.app

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277 <213> ORGANISM: Hordeum vulgare
 279 <400> SEQUENCE: 4
 280 ctcctgtgcc tgtcctgagg taccagaac accagtgaaa tggctgccca gaacaaccag 60
 281 gaggtggatg ccctgggta gaagatcacc gggctccatg cgcgaatcgc caagctgccg 120
 282 tcgctcagcc catccccggc cgtcgacgcg ctcttcacgg agctggtcac ggcgtgcgtt 180
 283 ccaccgagtc cagtggacgt gaccaagctc gggccggagg cgcaaggat gcgggagggc 240
 284 ctcatccgcc tatgctccga ggccgagggg aagctggagg cgactactc cgacatgctc 300
 285 gcccgcctcg acaaggcctg ggatcacctc ggcatgtcc cctactacaa caactacatc 360
 286 aacccatcgca agctcgagta cgagctcctg gcccgcctacg tgcctggcg 420
 287 gcgcgcgtcg cgttcatcg ctccggcccg ctgcccgttca gctcctttgt cctggccgcg 480
 288 cgcacacatgc cgcacacatgttgcacaac tatgacctgt gcggtgcggc caacgatcgc 540
 289 gccagcaagc tcttccgcgc ggatcgac gtgggtgccc gcatgtcg 600
 290 gacgtcgcgg acctcgccgg cgagctcgcc aagtacgacg ttgtcttctt ggcggcactc 660
 291 gtcggcatgg cgcggagga caaggcgaag gtgatcgcc acctcgccgc acacatggca 720
 292 gacggggcg 780
 293 gtcgacccccc aggacatcg 840
 294 gacgacgtgg tgaactccgt catcatcgca cagaagtcca aggacgtgca tgccgatgga 900
 295 cttggcagcg ggcgtggc 960
 296 ccccccgtgca gggtcgccg 1020
 297 tttgccaacg ccgaagtggc 1080
 298 tccatacctc gttctgtat tgcataa 1140
 299 tgcttctatc caataatgt 1200
 300 tgttacaag tgaattttaa ttccacaagta catataatgg tcaccattga aaagatgttt 1260
 301 agtgtgttt ttccaaatata tgtttgc 1320
 302 acccaaaaaa aaaaaaaaaa aa 1342
 305 <210> SEQ ID NO: 5
 306 <211> LENGTH: 335
 307 <212> TYPE: PRT
 308 <213> ORGANISM: Hordeum vulgare
 310 <400> SEQUENCE: 5
 311 Met Ala Ala Gln Asn Asn Asn Lys Asp Val Ala Ala Leu Val Glu Lys
 312 1 5 10 15
 314 Ile Thr Gly Leu His Ala Ala Ile Ala Lys Leu Pro Ser Leu Ser Pro
 315 20 25 30
 317 Ser Pro Asp Val Asp Ala Leu Phe Thr Glu Leu Val Thr Ala Cys Val
 318 35 40 45
 320 Pro Pro Ser Pro Val Asp Val Thr Lys Leu Gly Pro Glu Ala Gln Glu
 321 50 55 60
 323 Met Arg Glu Gly Leu Ile Arg Leu Cys Ser Glu Ala Glu Gly Lys Leu
 324 65 70 75 80
 326 Glu Ala His Tyr Ser Asp Met Leu Ala Ala Phe Asp Asn Pro Leu Asp
 327 85 90 95
 329 His Leu Gly Ile Phe Pro Tyr Tyr Ser Asn Tyr Ile Asn Leu Ser Lys
 330 100 105 110
 332 Leu Glu Tyr Glu Leu Leu Ala Arg Tyr Val Arg Arg His Arg Pro Ala
 333 115 120 125
 335 Arg Val Ala Phe Ile Gly Ser Gly Pro Leu Pro Phe Ser Ser Phe Val
 336 130 135 140
 338 Leu Ala Ala Arg His Leu Pro Asp Thr Met Phe Asp Asn Tyr Asp Leu

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; N Pos. 8
Seq#:23; Xaa Pos. 3,9,16,19,24
Seq#:24; Xaa Pos. 7,11
Seq#:25; Xaa Pos. 7
Seq#:26; Xaa Pos. 4
Seq#:28; Xaa Pos. 5,10
Seq#:29; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,12,13,16,17,18,19,20,21,23,24,26,27
Seq#:29; Xaa Pos. 29,31,32,33,34,35,36,39,40,43,44,46,48,49,50,51,54,55,56
Seq#:29; Xaa Pos. 57,58,59,60,62,65,66,69,70,72,73,76,77,80,82,83,84,85,87
Seq#:29; Xaa Pos. 88,89,91,94,97,98,102,103,106,107,109,110,113,114,117,118
Seq#:29; Xaa Pos. 119,120,121,122,123,124,125,126,127,128,131,138,139,141
Seq#:29; Xaa Pos. 142,145,146,149,150,151,152,154,156,157,158,159,160,161
Seq#:29; Xaa Pos. 164,165,167,168,170,171,172,173,174,175,176,177,178,179
Seq#:29; Xaa Pos. 182,184,186,187,188,189,190,191,192,193,194,196,197,198
Seq#:29; Xaa Pos. 206,210,211,212,213,215,216,217,218,219,222,223,226,227
Seq#:29; Xaa Pos. 230,232,233,234,235,236,237,238,240,245,247,248,249,250
Seq#:29; Xaa Pos. 251,252,253,254,257,260,262,265,266,267,269,272,273,274
Seq#:29; Xaa Pos. 275,276,278,279,280,281,282,283,284,285,286,287,288,289
Seq#:29; Xaa Pos. 290,291,292,293,294,295,296,297,298,299,300,301,302,303
Seq#:29; Xaa Pos. 304,305,306,307,308,309,310,311,312,313,314,315,316,317
Seq#:29; Xaa Pos. 318,319,320,321,322,323,324,325,326,327,328

VERIFICATION SUMMARY

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L:773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
M:341 Repeated in SeqNo=23
L:1242 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:1261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:1280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:1627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
M:341 Repeated in SeqNo=29